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0329



OIPF

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RAW SEQUENCE LISTING

DATE: 04/04/2002

PATENT APPLICATION: US/10/029,217A

TIME: 16:28:21

Input Set : A:\Utsd695.app

Output Set: N:\CRF3\04042002\J029217A.raw

3 <110> APPLICANT: OLSON, ERIC N.
4 WANG, DA-ZHI
6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO A CARDIAC-SPECIFIC
7 NUCLEAR REGULATORY FACTOR
9 <130> FILE REFERENCE: UTSD:695US
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/029,217A
C--> 12 <141> CURRENT FILING DATE: 2002-03-19
14 <150> PRIOR APPLICATION NUMBER: 60/257,761
15 <151> PRIOR FILING DATE: 2000-12-21
17 <160> NUMBER OF SEQ ID NOS: 32
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 4959
23 <212> TYPE: DNA
24 <213> ORGANISM: Mus musculus
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27 <221> NAME/KEY: CDS
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37 ctctgggctc ccgggagcca gtttctggtg gaaagcgggg cgcctggcca acgaccagcg 240
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43 accaaggctt aataccgcca ctgaaaggct caactgaatt ccatgacctg agaaaacaat 420
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51 gccaaaggccc ttggaactgg tggagaagaa cattctgccc atg gat tct tcc gtg 655
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53 1 5
55 aaa gag gct ata aaa ggt act gag gtg agc ctc tcc aag gca gca gat 703
56 Lys Glu Ala Ile Lys Gly Thr Glu Val Ser Leu Ser Lys Ala Ala Asp
57 10 15 20
59 gca ttc gcc ttt gag gat gac agc agt aga gat ggg ctc tct cca gat 751
60 Ala Phe Ala Phe Glu Asp Asp Ser Ser Arg Asp Gly Leu Ser Pro Asp
61 25 30 35
63 cag gct agg agc gag gac ccc cag ggc tct aca gga tcc acc cca gac 799
64 Gln Ala Arg Ser Glu Asp Pro Gln Gly Ser Thr Gly Ser Thr Pro Asp
65 40 45 50
67 atc aaa tcc act gag gct cct ctg gac aca atc cag gat ctc act cct 847
68 Ile Lys Ser Thr Glu Ala Pro Leu Asp Thr Ile Gln Asp Leu Thr Pro

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73	70 75 80 85			
75	tca gac cct ggg aag cag gtt ctc ggc ccc ctc agc acc ccg att cct	943		
76	Ser Asp Pro Gly Lys Gln Val Leu Gly Pro Leu Ser Thr Pro Ile Pro			
77	90 95 100			
79	gtg cac act gct gta aag tcc aag tct ttg ggt gac agt aag aac cgc	991		
80	Val His Thr Ala Val Lys Ser Lys Ser Leu Gly Asp Ser Lys Asn Arg			
81	105 110 115			
83	cac aaa aag ccc aaa gac ccc aaa cca aag gtg aag aag ctc aaa tac	1039		
84	His Lys Lys Pro Lys Asp Pro Lys Pro Lys Val Lys Lys Leu Lys Tyr			
85	120 125 130			
87	cat cag tac atc ccc cca gac cag aag gca gag aag tct ccc cca ccc	1087		
88	His Gln Tyr Ile Pro Pro Asp Gln Lys Ala Glu Lys Ser Pro Pro Pro			
89	135 140 145			
91	atg gac tct gcc tat gcc cgg ctg ctc cag caa cag cag cta ttc ctg	1135		
92	Met Asp Ser Ala Tyr Ala Arg Leu Leu Gln Gln Gln Gln Leu Phe Leu			
93	150 155 160 165			
95	cag cta cag atc ctc agc cag cag cag caa cag cag cag caa cag cag	1183		
96	Gln Leu Gln Ile Leu Ser Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln			
97	170 175 180			
99	cag cag caa cag cag cag cag cag cag cag cag cag cgg ttc agc tac cct	1231		
100	Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Arg Phe Ser Tyr Pro			
101	185 190 195			
103	ggg atg cac caa aca cac ctc aaa gaa cca aat gaa cag atg gcc aga	1279		
104	Gly Met His Gln Thr His Leu Lys Glu Pro Asn Glu Gln Met Ala Arg			
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107	aat ccg aat cct tct tca aca cca ctg agc aat acc cct cta tcc cct	1327		
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113	230 235 240 245			
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116	Gly Pro Leu Pro Pro Asn Leu Asp Asp Leu Lys Val Ser Glu Leu Arg			
117	250 255 260			
119	caa cag ctt cga atc cgg ggc ttg cca gtg tca ggc acc aag aca gcg	1471		
120	Gln Gln Leu Arg Ile Arg Gly Leu Pro Val Ser Gly Thr Lys Thr Ala			
121	265 270 275			
123	ctg gtg gac cgg ctt cgt ccc ttc cag gat tgt gct ggc aac cct gtg	1519		
124	Leu Val Asp Arg Leu Arg Pro Phe Gln Asp Cys Ala Gly Asn Pro Val			
125	280 285 290			
127	ccc aac ttt ggg gac atc aca act gtc acc ttt cct gtc acg ccc aac	1567		
128	Pro Asn Phe Gly Asp Ile Thr Thr Val Thr Phe Pro Val Thr Pro Asn			
129	295 300 305			
131	acc ttg ccc agt tat cag tcc tcc ccg aca ggc ttc tac cac ttt ggc	1615		
132	Thr Leu Pro Ser Tyr Gln Ser Ser Pro Thr Gly Phe Tyr His Phe Gly			
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135 agc aca agc tcc agc cca ccc atc tcc ccc gcc tca tct gac ttg tcc 1663
136 Ser Thr Ser Ser Ser Pro Pro Ile Ser Pro Ala Ser Ser Asp Leu Ser
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139 gct gca ggg tcc ctg cca gac acc ttc acc gat gcg tca cct ggc ttc 1711
140 Ala Ala Gly Ser Leu Pro Asp Thr Phe Thr Asp Ala Ser Pro Gly Phe
141          345          350          355
143 ggc ctg cac gca tct ccg gtg ccc gcc tgc acg gac gag agt ctg ctg 1759
144 Gly Leu His Ala Ser Pro Val Pro Ala Cys Thr Asp Glu Ser Leu Leu
145          360          365          370
147 agc agc ctg aat ggg ggc tcg ggc ccc tcc gag cct gat ggg cta gac 1807
148 Ser Ser Leu Asn Gly Gly Ser Gly Pro Ser Glu Pro Asp Gly Leu Asp
149          375          380          385
151 tct gag aag gac aag atg ctg gtg gag aag cag aaa gtg atc aac cag 1855
152 Ser Glu Lys Asp Lys Met Leu Val Glu Lys Gln Lys Val Ile Asn Gln
153 390          395          400          405
155 ctc acc tgg aag ctg cgg caa gag cag cgg cag gtg gaa gag ctg aga 1903
156 Leu Thr Trp Lys Leu Arg Gln Glu Gln Arg Gln Val Glu Glu Leu Arg
157          410          415          420
159 atg caa ctg cag aag cag aag agc agc tgc agc gac cag aag cca ctg 1951
160 Met Gln Leu Gln Lys Gln Lys Ser Ser Cys Ser Asp Gln Lys Pro Leu
161          425          430          435
163 ccc ttc ttg gcc acc acc atc aaa cag gaa gat gtc tcc agc tgc ccc 1999
164 Pro Phe Leu Ala Thr Thr Ile Lys Gln Glu Asp Val Ser Ser Cys Pro
165          440          445          450
167 ttc gca ccc cag cag gcg tct ggg aag gga cag ggc cac agc tct gac 2047
168 Phe Ala Pro Gln Gln Ala Ser Gly Lys Gly Gln Gly His Ser Ser Asp
169          455          460          465
171 agt ccc cct ccg gct tgt gag acg gct cag ctg ctg cct cac tgt gtg 2095
172 Ser Pro Pro Pro Ala Cys Glu Thr Ala Gln Leu Leu Pro His Cys Val
173 470          475          480          485
175 gag tcc tca ggt caa acc cat gta ctc tcg tcc acg ttt ctc agc ccc 2143
176 Glu Ser Ser Gly Gln Thr His Val Leu Ser Ser Thr Phe Leu Ser Pro
177          490          495          500
179 cag tgc tcc cct cag cac tcg ccc ctg ggg ggc ctg aag agc ccg cag 2191
180 Gln Cys Ser Pro Gln His Ser Pro Leu Gly Gly Leu Lys Ser Pro Gln
181          505          510          515
183 cac atc agc ctg cct cca tca ccc aac aac cat tac ttc ctg gct tcc 2239
184 His Ile Ser Leu Pro Pro Ser Pro Asn Asn His Tyr Phe Leu Ala Ser
185          520          525          530
187 tct tcg gga gct cag aga gag aac cat ggg gtc tct tca ccc agc agc 2287
188 Ser Ser Gly Ala Gln Arg Glu Asn His Gly Val Ser Ser Pro Ser Ser
189          535          540          545
191 agc caa ggg tgc gca cag atg act ggt tta caa tct tct gac aag gtg 2335
192 Ser Gln Gly Cys Ala Gln Met Thr Gly Leu Gln Ser Ser Asp Lys Val
193 550          555          560          565
195 ggg cca acg ttt tca att cca tcc cca act ttt tct aag tca agt tca 2383
196 Gly Pro Thr Phe Ser Ile Pro Ser Pro Thr Phe Ser Lys Ser Ser Ser
197          570          575          580
199 gca gtt tca gat atc acc cag ccc cca tcc tat gaa gat gca gtg aag 2431

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204 Gln Gln Met Thr Arg Ser Gln Gln Met Asp Glu Leu Leu Asp Val Leu
205      600      605      610
207 att gaa agt gga gaa atg cca gcc gat gcc agg gaa gat cat tca tgt 2527
208 Ile Glu Ser Gly Glu Met Pro Ala Asp Ala Arg Glu Asp His Ser Cys
209      615      620      625
211 ctt cag aaa att cca aag atc cct ggg tcc tcc tgc agc cca act gcc 2575
212 Leu Gln Lys Ile Pro Lys Ile Pro Gly Ser Ser Cys Ser Pro Thr Ala
213 630      635      640      645
215 atc ccc ccg aag ccc tcg gct tcc ttt gag cag gca tct tcg gga ggc 2623
216 Ile Pro Pro Lys Pro Ser Ala Ser Phe Glu Gln Ala Ser Ser Gly Gly
217      650      655      660
219 cag atg gcc ttc gat cac tac gcc aac gac agt gac gaa cac ctg gaa 2671
220 Gln Met Ala Phe Asp His Tyr Ala Asn Asp Ser Asp Glu His Leu Glu
221      665      670      675
223 gtc tta ttg aat tct cac agc ccc atc gga aag gtg agc gat gtt acc 2719
224 Val Leu Leu Asn Ser His Ser Pro Ile Gly Lys Val Ser Asp Val Thr
225      680      685      690
227 ctc ctc aaa atc gga agc gag gag cct cct ttt gac agc atc atg gat 2767
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231 ggc ttc cca ggg aag gct gcg gaa gat ctc ttc agt gct cac gag ctc 2815
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235 ttg cct ggg ccc ctc tcc ccg atg cat gca cag ttg tca cct cct tct 2863
236 Leu Pro Gly Pro Leu Ser Pro Met His Ala Gln Leu Ser Pro Pro Ser
237      730      735      740
239 gtg gac agc agt ggt ctg cag ctg agc ttc acg gaa tct cct tgg gaa 2911
240 Val Asp Ser Ser Gly Leu Gln Leu Ser Phe Thr Glu Ser Pro Trp Glu
241      745      750      755
243 aca atg gaa tgg ctg gac ctc act cca cct agt tcc acg cca ggc ttc 2959
244 Thr Met Glu Trp Leu Asp Leu Thr Pro Pro Ser Ser Thr Pro Gly Phe
245      760      765      770
247 agc aac ctt acc tcc agt ggg ccc agc att ttc aac atc gat ttt ctg 3007
248 Ser Asn Leu Thr Ser Ser Gly Pro Ser Ile Phe Asn Ile Asp Phe Leu
249      775      780      785
251 gat gtt aca gat ctt aat ctg aat tcc cct atg gat ctc cac tta cag 3055
252 Asp Val Thr Asp Leu Asn Leu Asn Ser Pro Met Asp Leu His Leu Gln
253 790      795      800      805
255 cag tgg taaacacccg aggtacaaga gctacgagag ctcaagtggga attcaatgga 3111
256 Gln Trp
258 ggaaagcacg ataccggaaa tgtgtgttcc aaaagatgaa ggggggaaaa tggggaggga 3171
260 aaaaaaaaaa cagcaacgga ggtttttgtg acaactaacc agaacaaaca gaagtcagct 3231
262 attaaaaatat gtctaaatgt aatatctacc agcattcagt aactgttaat aacttcagtg 3291
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266 atctcatacc agtttttttg ggtttttttt tgtttgtttt ttttttggtt tttttttttt 3411
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274 tcatcatcag tcagaagagc agggcctgtc tcaccaaatc gagtccttaa gacagaataa 3651
276 tcagaatggt cagagggaca gaccaatcaa ttcccaggaa agcaaaagtg actcaatgtc 3711
278 ccttgactcc caaatggtcc cactggactg gtgatcactg gtgacaacta actagctttg 3771
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310 gacaacatac agtttgcca aggcctcag aggccttgctg tggcgccaat tcaagtatta 4731
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314 caccaaggca ctgttttatt cttttgtaaa aaaaaaaaaa gttcactgtg cacttataga 4851
316 gaaaataatc aacaatgttg tgaatttttg agaagacttt tttttttttg ataaacaaaa 4911
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323 <212> TYPE: PRT

324 <213> ORGANISM: Mus musculus

326 <400> SEQUENCE: 2

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334 35 40 45
336 Gly Ser Thr Pro Asp Ile Lys Ser Thr Glu Ala Pro Leu Asp Thr Ile
337 50 55 60
339 Gln Asp Leu Thr Pro Gly Ser Glu Ser Asp Lys Asn Asp Ala Ala Ser
340 65 70 75 80
342 Gln Pro Gly Asn Gln Ser Asp Pro Gly Lys Gln Val Leu Gly Pro Leu
343 85 90 95
345 Ser Thr Pro Ile Pro Val His Thr Ala Val Lys Ser Lys Ser Leu Gly
346 100 105 110
348 Asp Ser Lys Asn Arg His Lys Lys Pro Lys Asp Pro Lys Pro Lys Val
349 115 120 125
351 Lys Lys Leu Lys Tyr His Gln Tyr Ile Pro Pro Asp Gln Lys Ala Glu
352 130 135 140
354 Lys Ser Pro Pro Pro Met Asp Ser Ala Tyr Ala Arg Leu Leu Gln Gln

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2305 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:2305 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:2506 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26